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Environment, Safety, and Health Directorate

WM-SVS

Administrative Procedure

HPGe System Gamma Spectroscopy Data Analysis

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REVISION HISTORY

Document Number and Revision *Include revision number, beginning with Revision 0*	**Effective Date** *Document Control Coordinator inserts effective date*	**Description of Changes** *List specific changes made since the previous revision*
AP-SWO-022, R.0	October 2001	This document supersedes DOP-54G-022, R.0.
AP-SWO-022, R.0	October 2002	No changes.
AP-SWO-022, R.1	May 2003	Comprehensively reviewed and revised for clarification.
AP-SWO-022, R.1.1	May 2003	Corrected errors on Page 5.
AP-SWO-022, R.2	June 2004	Incorporates the use of PeakDoctor as a spectrum fitting option. Also includes minor changes to SNAP™ V1.12.
AP-SWO-022, R.2.1	February 2005	Editorial changes, clarifications from walkdown for restart.
SWO-AP-0301, R.0	April 2006	New document number. Organizational name changes. Renumbered appendices and made other editorial changes. Replaced section 6.5 with steps for running the new version of PeakDoctor. Moved old section 6.5 to new Appendix B in case the previous Excel version of PeakDoctor is needed.
EP-AP-2203, R.0	April 2008	New document number. Organizational name changes.
WM-SVS-TP-008, R0	7/7/2016	Major Revision. Transfer of Ownership from EP to ADESH/WM. Remove references to Robwin software, add section on Radioassay Data Sheet, organizational name changes, and update references. Add PeakDoctor user guide as an appendix. This is a total rewrite and revision bars have been omitted.

Table of Contents

1.0 INTRODUCTION

The purpose of this administrative procedure is to describe the analysis of gamma spectroscopy data. This procedure specifies how gamma spectroscopy data are used to identify and quantify radioactivity in sample waste items.

2.0 SCOPE

This procedure applies to all personnel performing spectral analysis on data that have been previously collected using EP-DOP-2203, Operation and Calibration of Spectroscopy Systems, or EP-DOP-2207, Canberra Q2 Operations. The purpose of such data analysis is to identify and quantify the radionuclide content of assayed samples. This procedure describes the method of analyzing and reporting spectral data accepted by Los Alamos National Laboratory's (LANL's) Generator Services Team of the Waste Management Waste Services (WM-SVS) Group.

3.0 RESPONSIBILITIES

3.1 Team Leader

1. Ensures workers performing gamma spectroscopy analysis have completed the training requirements.
2. Ensures the quality assurance/quality control (QA/QC) measures described in this procedure are followed and the objectives of the QA/QC program are routinely achieved.

3.2 Supervisor

1. Ensures the gamma spectroscopy laptop computers are maintained in proper working condition.
2. Ensures the QA/QC measures described in this procedure are performed as required.
3. Periodically reviews reports to ensure the requirements of this procedure are being met.
4. Provides or supervises on-the-job training (OJT) for new personnel assigned to perform any portion of this procedure and maintains training documentation in accordance with LANL Procedure P781-1, Conduct of Training.
5. Updates this procedure as necessary and reviews this procedure as required.
6. Communicates to staff lessons learned or corrective actions taken to avoid reoccurrence of problems.
7. Ensures technical personnel maintain the required training.

3.3 Gamma Spectroscopy Analyst

1. Ensures high-purity germanium (HPGe) gamma spectroscopy analyses are performed in accordance with the requirements of this procedure.
2. Ensures documentation of analyses is maintained as required by this procedure.
3. Promptly reports all functional problems with the gamma spectroscopy software and/or laptop computers to the supervisor.

4. Maintains training pertinent to performing these duties as required.
5. Advises supervisor of necessary or desired changes to these procedures as a result of field experience or lessons learned.

4.0 PRECAUTIONS AND LIMITATIONS

- Do not overwrite or modify original spectra data files. Copies of original files can be made and the name of the file modified for analysis.
- When a worker observes an unsafe condition or act that may pose an imminent danger or other safety concern/hazard, the worker has the authority and responsibility to inform the worker engaged in the work and request that the work activity be paused and/or stopped based on the risk posed to the individual, the employees, the environment, or the facility in accordance with LANL Procedure P101-18, Procedure for Pause/Stop Work.
- N/A (not applicable) appears on the attachments to indicate information that is not required to be recorded during the performance of the procedure.
- The activities performed in accordance with this procedure are determined to be “low hazard” as defined by LANL Procedure P300, Integrated Work Management; therefore, no hazard analysis is required to perform this procedure.

Controls are to be established in order to ensure both the security of the data analysis and disaster recovery in case of a computer failure:

- Access to the data and analyses shall be limited to individuals authorized access (verbal or otherwise) by the WM-SVS Team Leader.
- The data and analyses shall reside on a LANL network folder.
- The use of a LANL network share provides disaster recovery through the process of network backup. The electronic backup, in conjunction with available paper (hardcopy) files, shall be used to re-create any lost data. Additional electronic records backup is provided through the Electronic Data Management System (EDMS).

5.0 PREREQUISITE ACTIONS

5.1 Planning and Coordination

Supervisor or designee:

1. Ensure that the current revision of this document is available, and identify this document as Working Copy or Information Only on the Title Page.

Note: Procedure may be performed by a trainee under the supervision of a qualified individual to allow the trainee to complete the training requirements.

2. Ensure that, as a minimum, two qualified individuals trained to the use of this procedure are available–one for primary analysis and one for independent review.

5.2 Materials and Equipment

Note: The list of materials and equipment is not an all-inclusive list, and additional tools and equipment may be used as necessary.

5.2.1 Special Tools and Equipment

Analyst:

1. Ensure that the following special tools and equipment are available, as required:
   - Log notes and desktop computers
   - Computer AC power adapter
   - Computer media (e.g., thumb drives)
   - Approved reference materials listed in section 8, References
   - Copy of Spectral Nondestructive Assay Platform (SNAP™) software
   - Copy of PeakDoctor, PeakEasy, ORTEC Maestro, or Canberra software for quantifying peak areas

6.0 PROCEDURE PERFORMANCE

Each subsection below is a standalone section and may be performed independently of or in conjunction with other procedure performance sections.

Note 1: Do not rely solely on gamma spectra for characterization.

Note 2: False results may occur because of

- high-matrix density
- large container size
- close detector-source distance
- centrally located activity with non-isotropic assay properties (hot spots)
- the absence of adequate spectral peaks (caused by high background or short count time)

Note 3: Such sources of error should have been minimized during the collection of the spectra. Review the gamma spectroscopy operator's record of the data collection, visually review the spectrum, and remain alert to anomalies during data analysis to determine whether the data are adequate to perform the analysis. Ask for clarification from the gamma spectroscopy operator and have the data collection redone if necessary.

Note 4: All gamma spectra discussed in this procedure have been previously acquired, saved, and logged into the logbook.

6.1 Transferring Background, Daily QC, and Sample Data Files

Analyst:

1. Ensure that the spectrum files (including background, daily QC measurements, and item/sample counts) have been copied to the Gamma folder on the server within several working days of generation. The files can be transferred from removable media or directly from the acquisition computer if it is connected to the network.
2. Ensure that the logbook pages applicable to the measurement have been scanned and copied in the Gamma folder on the server within several days of generation.

6.2 Preparing Gamma Spectral Data for Analysis Using PeakDoctor

Note: Step 6.2.21 presents information on manipulating the spectrum view. Step 6.2.21 can be performed at any time after a spectrum is loaded into the PeakDoctor software.

Analyst:

1. Double-click the PeakDoctor icon to open the software. The icon may be available as a shortcut on the computer desktop, pinned to the taskbar, or in the Start button programs listing.
2. Select the detector that collected the data from the Detector pull-down list.
3. If you know the spectrum type, then select the spectrum type from the Spectrum Type pull-down list. Otherwise, select the Background spectrum type from the Spectrum Type pull-down list.

Note 1: An optional energy calibration feature is available in PeakDoctor through the Energy Calibration On/Off button on the Main page. The button is green when activated and indicates Energy Calibration On; the button is grey when deactivated and indicates Energy Calibration Off.

Note 2: The energy calibration button may be set to either the On or Off mode when the PeakDoctor program is opened.

Note 3: If the energy calibration button is in the On mode, an energy calibration will be performed automatically upon opening the spectrum file. If the energy calibration is in the Off mode, no energy calibration will be performed upon opening the spectrum file.

4. If you are performing an initial energy calibration assessment, then
   a. click the energy calibration button until the button is grey and indicates Energy Calibration Off.
   b. click the Load Spectrum button (F10 key) to open a spectrum file.
   c. review the centroid of a low-energy calibration peak in the spectrum.
   d. review the centroid of a high-energy calibration peak in the spectrum.
5. If you determine that an energy recalibration on the spectrum is to be performed, then
   a. click the energy calibration button until the button is green and indicates Energy Calibration On.

b. select a low-energy recalibration peak from the Low Cal. pull-down list.

c. select a high-energy recalibration peak from the High Cal. pull-down list.

Note 1: The retrieval peaks step is automatically performed as soon as the spectrum is loaded.

Note 2: Hovering the cursor over major photopeaks allows viewing of the energy in the Energy (keV) box.

6. Open the spectrum file using the Windows Dialog box.

7. If you do not know the spectrum type, then view the spectrum to get a feel for which radionuclides are present.

8. Ensure that you have selected a spectrum parameter file (SPF) from the Spectrum Type pull-down list that most closely resembles the type of spectrum.

9. If you determine that it is necessary to change the default energy range, then change the default energy range over which to fit the spectrum as follows.

Note: A Warning box will appear when the energy range is changed.

a. Change the low-energy value in the Start Energy box.

b. Click Yes in the Warning box to accept the changed low-energy value.

c. Change the high-energy value in the End box.

d. Click Yes in the Warning box to accept the changed high-energy value.

10. If the fit peaks function is to be performed automatically, then

a. Ensure that the following have been achieved:

- Settings in the chosen SPF closely match the spectral features present in the current file (i.e., step peaks, Compton edge peaks (CEPs), etc.).
- Spectrum has a very precise energy calibration (you may use the energy calibration feature presented in step 6.24 to ensure this precision).

b. Press the One Step button (F12 key).

c. Review fitting results to ensure that the continuum and peak fits are acceptable, especially in regions where key photopeaks are located.

d. When the Choose File to Write dialog box appears, then click Ok to save the report file or click Cancel to discard the report file.

e. If the results were satisfactory, then go to step 6.22. Otherwise, proceed to step 6.11.

Note 1: Complete information on using and modifying Spectrum Parameter Files can be found in the PeakDoctor User Manual.

Note 2: The Undo button allows the user to go back one step for steps 6.2.11, 12, 13 and 14.

Note 3: The Reveal Peaks function starts automatically when a file is opened to begin the spectrum fitting process. However, if the default energy range is changed after the file is loaded, the Reveal Peaks function must be started manually by selecting the Reveal Peaks button.

Note 4: Peak channels will have a different color than the continuum channels.

11. Modify peak/continuum channels as needed using one of the following methods:

    a. Region of Interest (ROI) Peak Method

        • Left-click (once) at the starting point and at the end point.

        • Click the Set ROI Peak button or press the T key to change continuum channels to peak channels.

        • Click the Set ROI Cont button or press the G key to change peak channels to continuum channels.

    b. Edge Arrow Method

        • Click in the peak or continuum of interest.

        • Manipulate the Left Edge Arrow button or press the Z or X key and Right Edge Arrow button or press the C or V key.

Note: The following action changes a single peak channel to a continuum channel or a single continuum channel to a peak channel.

    c. Single-Channel Method

        • Click on the channel.

        • Click the Flip Point button.

12. Click the Fit Continuum button (F2 key).

13. Evaluate the fitting results.

Note 1: The following are common steps to enhance the continuum fit.

Note 2: The Improve Continuum button automatically changes all continuum channels to peak channels that are greater than 3 sigma above the residuals scale.

Note 3: The Improve Continuum button will override any manual continuum changes performed before clicking the button.

Note 4: The Spectrum Type page lists the available spectrum types and their associated step peaks (SPs), CEPs, backscatter energies (BSEs), and manual knot locations (MKLs). These can be adjusted as needed.

    a. Click the Improve Continuum button (F3 key) and re-click the Fit Continuum button.

    b. Add or remove SPs (Add SP/Rem SP buttons), CEPs (Add CEP/Rem CEP buttons), BSEs (Add BSE/Rem BSE buttons), or MKLs (Add Knot/Rem Knot buttons).

    Note: Knots can be viewed or hidden by pressing the Show Knots button (green reveals knots).

    c. Change additional peak and continuum channels as needed in accordance with step 6.2.11.

    d. Re-fit the continuum as many times as needed until the results are acceptable.

Note: The magnitude of the residuals scale can be modified at any time. A value of 3 to 5 sigma is generally adequate for most cases.

e. Quantitatively review the fit with the assistance of the residuals scale.

14. Click the Fit Peaks button (F4 key) to fit the spectrum photo peaks, and automatically generate a report.

Note 1: Take care not to overwrite the existing file when reviewing a spectrum that has already been adequately fit.

Note 2: If you desire, enter a different filename than the default.

15. When the Choose File to Write dialog box appears, then click Ok to save the report file or click Cancel to discard the report file.
16. View the spectrum peak-fitting results.
17. If any real peaks were not fit and you desire to include them in the report, then add the missed peaks to the report using the force peak routine:
    a. Hover the cursor over the peak centroid.
    b. Click once with the mouse.
    c. Click the Force Peak button (P key).
    d. Check the peak fit and adjust as necessary.

    Note: If the force peak routine doesn't work, turn off the Filter Peaks feature and repeat steps 17.a through 17.d.

    e. Click Ok to save the forced peak to the report file, as desired.
18. If the fitted peaks are to be removed, then
    a. go to the Peak Report page and click on the Report Data tab.
    b. place the cursor on the row containing the peak data to be removed.
    c. right-click anywhere on the row, and select Delete Element.
19. Click the Save Peak RPT button to save changes to the report data.
20. If ROI data is to be produced for a minimum detectable activity (MDA) calculation, then
    a. go to the MDA ROI page.
    b. click the check box on the left side of any row to automatically include that data on the MDA ROI report preview.
    c. double-click the empty cells to add rows below the default list and manually enter the different nuclide/photo peak pairs information, and verify that the nuclide, energy, and yield are accurately entered.

Note: The following step opens the Choose File To Write dialog box and allows the MDA ROI report to be saved.

d. Check-off as many rows as desired and click the Save button.

Note: The steps on manipulating the spectrum view presented in step 6.2 21 can be performed at any time after a spectrum is loaded into the PeakDoctor software.

21. Manipulate the spectrum view using the following guidance:

a. Click and drag from left to right to zoom the spectrum view.

b. Click and drag from right to left to expand the spectrum view back to the full working range.

c. Press the left or right arrow keys (← →) to move to the next section of the spectrum.

d. Press the Shift + arrow key to move left or right in smaller increments.

Note: Pressing the Shift key with the arrow key changes the vertical scale in smaller increments.

e. Press the up-arrow key (↑) to increase the vertical scale, and press the down-arrow key (↓) to decrease the vertical scale.

f. Click the Log/Linear button to toggle between those scales.

Note: The technique in the following step can be useful for detecting very small photopeak fluctuations.

g. Click the Zero Suppress button to change the view so the channel with the fewest counts is positioned at the bottom of the view.

22. Click the Exit button to close PeakDoctor.

6.3 Preparing Gamma Spectral Data for Analysis Using ORTEC Maestro

Note 1: Maestro can also be used to add or subtract two or more spectrum files. For example, the background can be subtracted using the Calculate/Strip command. Files can also be added using the Calculate/Strip command with a stripping factor of -1.0. This command is commonly used to perform spectral summing (see section 8, References, for additional details on spectral summing applications).

Note 2: The Maestro buffer screen appears in the following step.

Analyst:

1. Double-click on the Maestro icon (or use Start, All Programs, Maestro 32, Maestro for Windows).

Note: The standard Windows Search screen appears in the following step.

2. Click on File, Recall.

Note: The following step will load the spectral file into the buffer.

3. Locate your file (mmddyy##.chn) and Click on Open.

Note: The program will highlight the ROIs at each of the located peaks in the following step.

4. Click on Calculate, Peak Search to perform a peak search.

Note: The ROI Report screen appears in the following step.

5. Click on File, ROI Report.

6. Check the Print To File box.
7. Check Column in the Format box.

Note: A Windows Report File screen appears in the following step.

8. Click Ok.
9. Store the report file into the same folder that the *.chn file came from.

6.4 Preparing Gamma Spectral Data for Analysis Using Genie-2K

6.4.1 Performing a Batch Routine Analysis on the Background File

Note: The Background Analysis 3 shortcut is used when maximum sensitivity is required (this will be most of the time).

Analyst:

1. Double-click on the desired Background Analysis icon.

Note: The batch procedure will prompt the following:

2. Enter name or initials and click the Ok button.
3. Select the appropriate background file to be analyzed, and click the Ok button (refer to logbook for filename as necessary).

Note: The batch procedure will automatically analyze the file, save the file, and display the report on the computer screen for review.

4. Click the Ok button to save the parameters and start the analysis.
5. Click the End View button to remove the report from the computer screen.

6.4.2 Perform Batch Routine Analysis on the Sample File

Note: The program requires that files for analysis be ordered sequentially and that the background subtraction routine be used. Be sure that all spectrum files and the Gamma Acquisition and Analysis software are closed.

1. Double-click on the desired Routine Sample Analysis icon.
2. Enter name as prompted by the batch procedure.
3. Click the Ok button.
4. Enter the number of sample files to be analyzed in the entry field that appears.
5. Select the first sample file to be analyzed and click the Ok button.
6. When the batch procedure displays Use Background Subtraction?, then select Yes.
7. Select the appropriate background file and click the Ok button.

Note: The batch procedure will automatically analyze the file and save the report.

8. Click the Ok button to save the selections and start the analysis.

6.5 Analysis of Sample Spectral Data Using SNAP™

6.5.1 Identify Radionuclides

Knowing the waste generation process will help you identify the radionuclides present in your items. In addition, the peak identification process tends to move along more quickly when the largest peaks in the spectrum are identified first along with secondary peaks associated with the same isotope. Major contaminants will often have two or more gamma-ray peaks present in the spectra. Attachments 2 and 3 contain lists of common background and sample peaks, respectively.

The size of secondary peaks from the same isotope relative to the primary peaks will be affected by several criteria:

- the relative gamma-ray yield per decay
- the relative gamma-ray energy and change in intrinsic efficiency
- the relative attenuation losses due to effective matrix density, wall thickness, and matrix and wall materials
- relative counting statistics

Once the majority of radionuclides have been qualitatively determined, you are ready to use SNAP™ to complete the peak identification process:

a. Determine if the identified peaks are real or a result of statistical fluctuations in the continuum.

b. Determine if any valid peaks have not been identified during the peak search routine.

c. If valid peaks have not been identified, re-run the peak search routine with a lower sensitivity threshold or manually add the peak data to SNAP's RPu file.

Analyst:

1. Visually review the spectra using PeakDoctor, PeakEasy, ORTEC Maestro, or Genie-2K to determine the radionuclides that are present.
2. Double-click the SNAP icon to launch the SNAP™ software. The icon may be available as a shortcut on the computer desktop, pinned to the taskbar, or in the Start button programs listing.
3. Click the yellow Identify Nuclides button to identify the nuclides.

Note 1: If the file type you open does not match the type you have chosen, an error message will appear. Be sure to enter the correct file type (starting with the background file is recommended). If you get an error message, redo the step with the proper file type selected.

Note 2: PeakDoctor uses the Robwin file type.

4. Click the format of the data file in the File Type box.
5. Click the white Search For File button, and use the dialog box to locate and open the desired file.

Note: While it is possible to disable the energy calibration feature by clicking on the green Energy Calibration On button, it is <u>not</u> recommended unless the energy calibration has already been done in PeakDoctor. When disabled, the button will be colored grey and indicate Energy Calibration Off.

6. If an energy calibration modification is to be performed, then verify that neither of the Spectrum Energy boxes within the Energy Calibration box is flashing red (calibration questionable); if an energy calibration modification is not to be performed, disable the energy calibration button and go to step 6.5.1.8.
7. If one or both of the Spectrum Energy boxes are flashing red, or either of the peak energies in the Spectrum Energy boxes is not the intended value, then
   a. locate a known peak energy in the Input Data box.
   b. click on the drop-down list in the corresponding Real Energy box, and select the correct identity from the list for the known peak energy.

Note: The recommended peaks to use for the energy calibration are the Pb-Ka1 x-ray at 74.97 keV and the K-40 1460.8-keV gamma ray. Both are usually present in a spectrum and have relatively good statistics. If one or both are not present, choose other peaks so that the energy calibration is done using one lower-energy peak and one higher-energy peak.

   c. If both Spectrum Energy boxes are flashing red, then repeat step 6.5.1 7b.

8. Choose a library:
   a. If the nuclides are known, then choose a library according to the nuclides expected to be present in the spectrum.
   b. If the nuclides are completely unknown, then choose Full.

Note: Instructions for creating a new library are in section 6.7.5.

   c. If none of the libraries fits the current situation, then create a new library or use the full library.

Note: The following step saves a lot of time during peak identification.

   d. If there are multiple similar spectra, then create a new library that fits the spectra.

Note 1: If a new library was created, the new library is to be selected in the Library box after editing the Edit Libraries dialog.

Note 2: Checking the Exclusive box may result in numerous unknown peaks in the report if the library does not match very closely the actual peaks present. In such a case, checking the Fallthrough box, modifying the selected library, or selecting another library may produce better peak ID results.

9. If the peaks come from one specific library, or the peaks that do not match the chosen library are to be labeled as unknown, then check Exclusive in the Search Options box.

Note: The search routine in the following step falls through the selected library to the full library.

10. If peaks are to be identified when no match is found from the library chosen, then check the Fallthrough box.

Note: The Exclusive and Fallthrough boxes are disabled if the full library is chosen.

11. Choose whether to partially or fully automate the ID process as follows:

Note: In the semi-automated mode, the computer asks for help only in cases when more than one match for a peak is found in the library.

a. Check the Semi-Automated Mode box to partially automate the ID process and limit the amount of user interaction required.

Note 1: The following fully automates the search.

Note 2: The background of the Input Data box will turn a pale yellow and the label will change to Output Data, indicating completion of the ID process, if the Fully-Automated Mode option is checked. You can then proceed to step 6.5.1 16.

b. Check both the Semi-Automated Mode and The Fully-Automated Mode box to eliminate user interaction completely.

12. Click the yellow Identify Peaks button (F4).

Note: The identification process will proceed from the lowest energy to the highest energy.

13. When the Choose A Suggestion window appears, then double-click the appropriate response or the Continue (F1) button.

Note: Unidentified peaks may result from fluorescence x-rays, sum peaks, prompt neutron capture gamma rays, and single or double escape peaks. Other possibilities for unidentified peaks are that the energy match tolerance needs to be increased, that the calibration needs to be adjusted, or that the peak is not in the chosen library.

14. If the sample peaks remain unidentified after performing the previous steps, then determine the cause of unidentified peaks.

Note: It is occasionally acceptable to leave peaks labeled as UNK (unknown) if their origin cannot be determined or if they are unimportant low-abundance gamma rays not included in the SNAP™ library.

15. Repeat steps 6.5.1.9 through 6.5.1 14 (deductive evaluation process) until all sample peaks have been appropriately identified.

Note 1: The Choose A Suggestion window should no longer appear, and the Input Data box should turn pale yellow.

Note 2: Peak IDs may be manually changed in the Output Data Box; however, this requires that the peak yield be changed too.

Note 3: Even if the Fallthrough box was checked, changes may be made to the results, or the desired peaks may be added to the library, when peaks are labeled unknown because no matching peak was found in the libraries.

16. Review the work in the Output Data Box and make any necessary changes or corrections (for example, identify peaks that SNAP™ labeled as unknown).

17. If the peak identification process is to be re-performed, then click the Reset (F12) button.

Note: The background file must go through the peak identification process before it is subtracted.

18. If a peak background subtraction is to be performed before saving the RPu file, then perform the following:
    a. Click on the white BKG Subtract button.
    b. When the Windows Open screen appears, then select the background RPu file containing the peak background data and click the Open button.
    c. When the Enter Count Durations screen appears, then perform <u>one</u> of the following:
        - If the background count and the sample count are the same, then click the Count Durations Equal? button until it indicates Yes; then go to step 6.5.1 18e.
        - If the background count and the sample count are <u>not</u> the same, then click the Count Durations Equal? button until it indicates No.
    d. Enter the sample count time and the background count time in the appropriate box.
    e. Click the Continue button.

19 If the peak ID dialog process is to be repeated, then click the red Reset (F12) button and return to the desired step in section 6.5.1.

20. If you are satisfied with the peak identification just completed, then click the flashing yellow Save to RPu File button to save the newly created MMDDYY##.RPu file or MMDDYY detectorname##.RPu file.

21. If you are completing the peak identification process for the first background file of the day, and you desire to hide the background nuclides on the assay calculations, then click the white Reset BGn File button.

6.5.2 The Container Modeling Process

Note 1: The Identify Nuclides window will disappear, and the Modeling Data window will appear after you click on the yellow Modeling Data (F1) button.

Note 2: Complete the Modeling Data page cells by following the directions below.

Analyst:

1. Click the yellow Modeling Data button to go to the Modeling Data page.

Note: The item description in the following step is available from the detector's logbook. Attachment 4, Logbook, provides details on the information contained in the logbook.

2. Enter a description of the item (e.g., barcode and container type) in the Description box.

Note: The ID of the most recent spectrum from which peaks were identified will automatically appear in the File ID box if the Modeling Data window is opened immediately after performing the peak identification.

3. Enter the ID number of the file containing the data to be modeled in the File ID box, <u>or</u> use the Search for File button to browse and find the file containing the data to be modeled.

Note: Normally English units are used.

4. Choose either English or Metric units in the Length/Weight Units box.

Note: Normally Ci units are used for activity units.

5. Choose the activity units in the Activity Units box.

Note: Normally nCi/g units are used for concentration units.

6. Choose the concentration units in the Concentration Units box.

Note: SNAP™ has several common container parameters pre-defined in a Custom Models library.

7. If a SNAP™ common container is applicable, then
   a. Click the Choose/Edit Custom Models button to automatically enter the physical dimensions of the common containers.
   b. Go to step 6.5.2 12.
8. Choose box, cylinder, area source, or linear source in the Model Type box.
9. Enter the container vertical dimension or the vertical height of the matrix inside the container (if known) in the Height box.
10. Enter the container width in the Width box.

Note: The Width box is labeled Diameter if a cylinder is chosen for the Model Type.

11. Enter the container depth in the Depth box.

Note: The Depth box will be grayed if a cylinder is chosen for the Model Type.

12. Enter the distance between the face of the detector and the point on the container (or effective matrix volume) along the detector's axis of radial symmetry in the Detector To Item Distance box.
13. Enter the vertical distance between the bottom of the sample matrix and the center of the detector crystal in the Detector Height box.

Note: Negative distance is used in step 6.5.2 14 if the detector was to the right of the center.

14. Enter the horizontal distance between the center of the detector crystal and the horizontal center of the container in the Left of Center box.
15. Select the name of the detector used in the Detector Calibration box.
16. Choose the shielding configuration in the Angular Correction box.
17. Choose the primary matrix material from the Primary Matrix Material box.
18. If only <u>one</u> attenuating material is to be used, then
    a. Set the primary matrix fraction (%) in the Primary Matrix Fraction (%) box to 100.0.
    b. Go to step 6.5.2 21.

Note: The remainder of the matrix is composed of the secondary matrix material.

19. Set the primary matrix fraction (%) in the Primary Matrix Fraction (%) box to the volume fraction of the matrix composed of the primary matrix material.

Note 1: The Secondary Matrix Material box is grayed if the Primary Matrix Fraction (%) box is set to 100.0%.

Note 2: The secondary matrix fraction applied is (100%–Primary Matrix Fraction [%]), if the Primary Matrix Fraction (%) box is set to less than 100.0%.

20. Choose the secondary matrix material from the Secondary Matrix Material box.

Note: The Matrix Weight/Packing Efficiency box tells SNAP™ how to calculate the effective density of the matrix.

21. Set the contents to either Matrix Weight or Packing Efficiency in The Matrix Weight/Packing Efficiency box to direct the matrix density calculation:
    a. Choose Matrix Weight to instruct SNAP™ to interpret the contents of the box to be the net weight of the matrix and to use this information with the volume of the container to calculate the effective density of the matrix.
    b. Choose Packing Efficiency to instruct SNAP™ to calculate the weight of the matrix using the volume and material density.

Note: The Item Weight box is active only when air is the primary matrix material and SNAP™ automatically calculates weight of the air as the matrix weight. An example would be a glovebox or some other hollow item. The purpose of the Item Weight box is to allow the correct calculation of concentration of surface contamination.

22. If air was set as the primary matrix material, then enter the weight of the item in the Item Weight box.

Note: The primary wall is usually the wall closest to the matrix that is part of the container encasing the matrix.

23. Enter the primary container wall thickness in the Primary Wall Thickness box.
24. Choose the primary wall material in the Primary Wall Material box.
25. Enter the secondary wall thickness, or the thickness of a cadmium shield or other attenuator used, in the Secondary Wall Thickness box, as applicable.
26. Choose the secondary wall material in the Secondary Wall Material box.
27. Enter the tertiary container wall thickness, or the thickness of any other attenuator used, in the Tertiary Wall Thickness box.
28. Choose the tertiary wall material in the Tertiary Wall Material box.
29. Enter the amount of detector live time for the count in the Count Time (sec) box.

Note 1: The altitude information is used to calculate the density of air, which is necessary to correct for the attenuation losses of gammas in air between the item and the detector.

Note 2: The altitude usually used for Los Alamos is 7000 ft.

30. Enter the altitude at which the count was performed in the Altitude box.

    Note: The MDA level is usually used for the detection limit.

31. Choose whether you want to report MDAs or activity Critical Levels of Detection in the Detection Limit box.

    Note: Application of a rate-loss correction must have documented technical justification.

32. Enter the rate-loss correction factor in the Rate Loss Correction Factor box, as applicable.

    Note 1: There is currently no provision for a 1-sided count. If you are modeling a 1-sided count, then select a 2-sided count.

    Note2: If an item is rotated 360 degrees during the count, choose the 4-sided count.

33. Choose either a 2- or 4-sided count in the GA Error #Sides box, according to number of sides from which the item was counted.

34. Choose the analyst's name from the drop-down list in the Analyst box.

    Note 1: Once a complete model is defined, it can be saved as a custom model to be used in subsequent analyses by clicking the Save Custom Setup button, naming the ".ini" file, and clicking Save.

    Note 2: To retrieve custom model parameters, click the Load Custom Setup button, select the desired custom model, and click Open. All model parameters set during the creation of the selected ".ini" file will thereby be recalled and returned to the model page.

    Note 3: After recalling a custom setup, confirm that all the model parameters retrieved are applicable, and change and correct as needed.

6.5.3 The Assay Calculations Process

Analyst:

Note: If you wish to perform special modeling, isotopics, or transmission corrections, refer to section 6.7, SNAP™ Special Features.

1. Click the yellow Assay Calculations (F1) button to go to the Assay Calculations page.
2. If the Assay Calculations window was entered directly from entering data into the Modeling Data window, then the correct spectrum ID is displayed in the File Name box.

Note 1: The Search for File and Load from File buttons are used for changes in the directories from the last time that the Assay Calculations window was used.

Note 2: If the white Reset BGn File button on the Identify Nuclides window was clicked, then the green Remove BG Nuclides On button may be clicked to hide the nuclides present in the item count spectrum that are also present in the background. Clicking on the Remove BG Nuclides On button will turn it gray and change its label to Remove Background Nuclides Off.

Note 3: In the Assay Calculations window, load only files with the *.RPu suffix.

3. If the Assay Calculations window was not entered directly from entering data into the Modeling Data window, or the Nuclides box is empty, then use the Search for File and Load from File buttons to locate the correct file.

4. Highlight desired peaks for calculation in the Nuclides box.

Note: You can highlight multiple peaks by holding down the Shift key while clicking.

5. If a graphical differential peak analysis using the View Curves window is to be performed, choose only peaks from only one nuclide (or with daughters in secular equilibrium).

Note: Activities will be calculated and the results displayed in the table at the bottom of the window.

6. Click on the Calculate Activity (F4) button after the desired peaks have been highlighted.

7. Compare the results from different energy peaks for the same nuclide to see how well they agree.

8. If the peaks agree reasonably well, then go to section 6.5.4, completing the SNAP™ Report.

Note1: The View Curves window appears in the following step.

Note 2: The View Curves window graphically displays the relative amounts of contamination SNAP™ calculates from different energy peaks for the same nuclide. This feature is particularly useful when there is a need to perform a lump correction for uranium or plutonium but can also be used to identify outlier or suspect peaks that should be discarded.

Note 3: It is important to choose only peaks from the same nuclide (or with daughters in secular equilibrium) in the Nuclides box when using the View Curves window.

9. If there is more than one peak per nuclide to be compared graphically, then click the yellow View Curves button.

   a. Resize the vertical scale, if desired, by clicking on the small Y in the gray box.

Note: Sometimes a lump correction for uranium or plutonium is necessary. Usually a half-gram or more of uranium or plutonium must be present in the container for a lump correction to be justified.

   b. Choose uranium or plutonium in the Lump Correction box, as appropriate, to perform a lump correction.

Note 1: The initial value in the following step is an initial guess at the equivalent thickness of the lumps.

Note 2: A value between 100 and 1000 microns is a good initial estimate.

   c. Enter an initial value into the Thickness (Microns) box.

   d. Click the Apply Lump Correction button.

   e. If the low-energy peaks are under-attenuated (that is, below the average activity line), then increase the thickness and go to Step 6.5.3 9d.

f. If the low-energy peaks are over-attenuated (that is, above the average activity line), then Decrease the thickness and Go to Step 6.5.3 9d.

10. Repeat Steps 6.5.3.7 through 6.5.3 9f until all of the chosen peaks are in reasonably good agreement with each other.

Note: An example of a case requiring the performance of step 6.5.3 10 is an item containing Am-241, Pu-239, Pa-233, Co-60, and Cs-137 with good Pu-239 counting statistics. In such a case, determine the size of the lump correction using only the Pu-239 peaks. Considering one nuclide at a time, check if multiple energies (if available) of the non−Pu-239 nuclides result in similar activity levels. If so, applying the lump correction is appropriate for the non-plutonium nuclides as well as the Pu-239.If not, then the lump correction should be applied only to the nuclides that do show similar activity levels for multiple energies.

11. If a radionuclides lump correction is to be applied to all of the results, then

    a. return to the Assay Calculations window and choose all of the other peaks that the lump correction is to apply.

    b. click the Calculate Activity (F4) button.

    c. click Yes in the screen asking whether to apply the lump correction to the results.

Note 1: Step 6.5.3.12 will erase the amount of the lump correction in the final report, so note the lump correction amount and the nuclides that the lump correction was applied to in the Note: section of the report tab.

Note 2: A graphical differential peak analysis can also be done for other radionuclides.

12. If a peaks lump correction is to be applied to a portion of the results, then

    a. return to the Assay Calculations page.

    b. click on the yellow Reports (F1) (Save Changes) button to save the first set of results.

    c. on the Reports page, click the green Add More Results button.

    d. highlight the peaks that will not get the lump correction.

    e. click the Calculate Activity (F4) button; the results will be added to the Reports page as described in section 6.5.4.

6.5.4 Completing the SNAP™ Report

Analyst:

1. Proceed to the Reports screen by clicking the yellow Reports (F1; Save Changes) button. If you need to make changes to the modeling data on the Report screen, click the green Return (F2) button. Click the green Add More Results button if you need to add more results to those you have already calculated (e.g., if you want to apply a lump correction to some results and not to others, or if you want to add MDA calculations).
2. Review the values displayed on the Reports screen.
3. If the report values displayed are not satisfactory, then click the green Return (F2) button.

Note 1: The total 2 sigma error is the total of three counting errors summed in quadrature (geometry and attenuation error, counting statistics error, and detector error). In most counting situations, the geometry and attenuation error is the largest of the errors. SNAP™ determines this error by calculating what the potential activity variation would be if all the activity in the container were located at a single point in the worst volume position. Large containers with high densities create the greatest variances, especially for isotopes identified via low-energy peaks.

Note 2: It is apparent that the total 2 sigma error grossly overestimates the actual analysis error when the container matrix is well characterized and the activity is known to be uniformly distributed. A container is well characterized when one or more of the three conditions listed below occur:

- A good activity agreement is observed (that is, within 20%) in the differential peak analysis between peak activity determinations for a single nuclide that has gamma emissions greater than 300 keV apart.
- The material matrix is known to be homogeneous (for example, soil or resin).
- Dose-rate information is measurably above background and uniform around the container.

Note: 3: The editing in step 6.5.4 4 can be performed only on the currently calculated errors. If the Add More Results button has been used, previously calculated errors cannot be changed.

4. Edit the calculated 2 sigma error by clicking on the Edit Error Estimates box, as necessary.
5. Document comments in the Notes box of the Reports page to describe any unusual circumstance of the assay count or the analysis or to note information that will help the reviewer perform the review.
6. Click the blue View Errors button to see a listing of the individual errors for each isotope, as necessary.
7. Check the Include RPu? Box to include the peak identification in the printed report.
8. When the Reports page is complete, click the Print Report (F4) button and the Save Report button.
9. Click the green Return (F2) button to go back to the desired SNAP™ page.

6.5.5 The MDA Calculation Process

Note: Section 6.5.5 needs to be performed only if MDAs are required for the final report.

Analyst:

1. Click the Calculate Detection Limits button on the Assay Calculations page.
2. If the MDA is to be calculated from a previously saved MDA file in *.RPu format, then
   a. click the green Return (Get Sets From RPu File) button to retrieve an MDA file previously saved in PeakDoctor.
   b. go to step 6.5.5.7.

   Note: A rule of thumb for the number of channels to use to calculate the background counts is to use a value equal to three times the full width at half-maximum (FWHM) at that energy.
3. Determine the background counts for each peak location representing the isotopes selected for MDA analysis (for example, 129.29 keV for Pu-239).
4. Select a pre-established set of MDA peaks representing the desired MDA isotopes on the Calculate Detection Limits screen or use the gray buttons on the bottom of the screen to build the desired set of MDA peaks.
5. Click the green Return (use selected Sets) button.
6. Enter the background counts for each MDA-peak you wish to evaluate (not all peaks in the set need to be evaluated) into the Calculated Detection Limits table, and click Return.
7. Review the MDA values displayed on the Assay Calculations page.
8. If the MDA values are not satisfactory, click the Calculate Detection Limits button and repeat steps 6.5.5.2 through 6.5.5.7 until you obtain satisfactory data.
9. Click the Reports (F1) (Save Changes) button.
10. Click the Print Report (F4) button on the Reports page.
11. Document comments in the Notes box to describe any unusual circumstance of the assay count or the analysis or to note information that will help the reviewer perform the review.

    Note: A copy of a completed report is shown in Attachment 5, Sample Gamma Spectroscopy Report Format.
12. Click the Save Report button.
13. Click the Return (F2) button to go back to the desired SNAP™ page.

6.6 RADIOASSAY DATA SHEET

Note: Some of the steps in section 6.6 may be skipped if you are revising a previously saved version of the spreadsheet.

Analyst:

1. Obtain a batch data report (BDR) number from the gamma spectroscopy supervisor (e.g., LALLW1234) or from the FileMaker (FM) database.
2. Open the Excel spreadsheet that generates a radioassay data sheet (RDS) file–SNAP05C_Gamma (or current version).
3. Click the Set Preferences button on the main menu screen to check or reset the preferences, as necessary.
4. Click the Reset All Values button on the main menu screen of the spreadsheet to ensure that the spreadsheet is cleared of previous data.
5. Save the spreadsheet with the addition of the BDR number (e.g., SNAP05C_Gamma_LALLW1234) as a macro-enabled workbook (*.xlsm format).
6. Click the Load Electronic File button on the main menu screen of the spreadsheet.

   Note: *.txt or Excel files can also be loaded using this button.
7. Select the *.htm file(s) to load into the spreadsheet.
8. Click the RDS Review, Print, Upload button on the main menu screen of the spreadsheet.
9. Click the Select Drum button on the RDS screen of the spreadsheet.
10. Select the container to be evaluated by the spreadsheet.
11. Click OK.
12. Input the BDR number on the RDS screen (e.g., LALLW1234).

    Note: Several plutonium and uranium material types (MTs) are available in the RDS screen. The G sheet of the spreadsheet shows the weight percentages of the various isotopes in each of these MTs near the bottom of the sheet.
13. Review the nuclide data on the RDS screen, and click on the appropriate MT button to choose a plutonium and/or uranium MT, as applicable.
14. Click the GO button on the RDS screen to calculate MDAs for undetected isotopes for the MT selected.

    Note: For step 6.6.15, preset the folder path for the location to which the flat file is to be saved using the SaveFlatFilePath in the Set Preferences tab.
15. Click the Load RDS to Server button on the RDS screen to save a copy of the text file for this container.

    Note 1: The printed report is to be included in the report to the generator for this container.

    Note 2: Adobe PDF must be set as the default printer in Windows.
16. Click the Print RDS button on the RDS screen to print a *.pdf version of the RDS for this container.
17. Resave the spreadsheet so that the current loaded spectral data is saved.

18. If the assay data is not part of a standard gamma spectroscopy report, then prepare a BDR cover sheet (BDR LALLW####.xls).

Note 1: Step 6.6.19 must be performed by a person with access to the FileMaker program and the FileMaker nondestructive assay (NDA) Master database.

19. Input the data to the FileMaker NDA Master database.

6.7 SNAP™ SPECIAL FEATURES

Note: Steps in section 6.7 are optional, to be performed as needed.

6.7.1 Special Modeling

Note: Refer to the SNAP™ User Manual to learn to save special modeling information.

Analyst:

1. Click the blue Special Modeling button from the Assay Calculations screen.

Note: You may recall previously created custom weighting factors (WFs) as desired.

2. Select the WF type (Point Source, Transverse Slice, or Horizontal Slice) on the Special Modeling screen.
3. Enter the WFs so that WFs reflect the contamination distribution within the container.
4. Click the green Return button.

6.7.2 Plutonium Isotopics Function

Plutonium isotopics is the determination of isotopic content by percent mass and percent activity using the spectral data. For the plutonium isotopics subroutine to function, it is important that certain key photopeaks are present in the spectrum and that the nuclides have been properly identified. As shown in the table below, the spectrum must contain a 169.56-keV gamma ray from Am-241 and have the 160.28-keV gamma ray of Pu-240 well resolved from the 161.45-keV gamma ray of Pu-239. The 161.45-keV gamma ray of Pu-239 is not used for the isotopics subroutine, but it must be well resolved from the 160.28-keV gamma ray of Pu-240 to avoid an error in the number of counts in the 160.28-keV gamma ray. Furthermore, the 164.58-keV gamma ray must be identified as belonging to U-237 as opposed to Am-241.

Isotope	keV
Am-241	125.292 (E_1)
Pu-239	129.294 (E_2)
Pu-239	144.211 (E_3)
Pu-241	148.567 (E_4)
Pu-238	152.68 (E_5)
Pu-240	160.28 (E_6)
U-237	164.58 (E_7)
Am-241	169.557 (E_8)

Note: Modeling data are irrelevant to isotopics calculations.

Analyst:

1. Click the blue Isotopics button from the Assay Calculations screen.

Note: All the photopeak data for Pu-239 will be displayed in the following step.

2. Go to the Isotopics Select box and choose Fissile Pu on the right-hand side of the Isotopics page.

Note 1: Commonly used gamma-ray peaks include the following: 129.29, 144.21, 161.45, 203.54, 255.38, 345.01, 375.04, 413.71, and 451.47 keV.

Note 2: Highly elevated Am-241 in the sample could add additional uncorrected counts in the 203.54-keV peak. Elevated Pa-233 could do the same in the 375.04-keV peak.

3. Create the relative efficiency versus energy curve by selecting a minimum of five photopeaks with good counting statistics.

Note 1: The isotopic results will be displayed in the following step.

Note 2: If any of the photopeaks used in the calculation have less than 1000 net counts, a warning will show on the screen stating “Poor counting statistics in some peaks may yield inaccurate results.” This warning does not mean that the results cannot be calculated; it simply advises that the results may not be as good as desired. Note receipt of this warning in the comments section of the report.

Note 3: If the E6, E7, and E8 peaks shown above in the table are not available or properly identified, an error message will appear on the screen stating “Peak(s) not found to do calculation,” and the isotopic calculation cannot proceed.

Note 4: You can save and/or print the report.

4. When the relative efficiency curve has been created to your satisfaction, click the yellow Calculate Isotopics button.

6.7.3 Uranium Isotopics Function

Note 1: Uranium isotopics is the determination of isotopic content by percent mass and percent activity using the spectral data. The uranium isotopics function in SNAP™ works only for low-enriched uranium, natural uranium, or depleted uranium samples. An isotopics function for highly enriched uranium is not available.

Note 2: The 143.79-keV peak for U-235 is the key photopeak used to determine the U-235 percentage. To perform uranium isotopics, the spectrum must have a well-formed 258.18-keV photopeak from Pa-234m, as well as either a 92.57-keV or 63.29-keV photopeak from Th-234.

Analyst:

1. Proceed directly to the Assay Calculations screen after nuclide identification is complete. Click the blue Isotopics button.

Note 1: Modeling data is irrelevant to isotopics calculations.

Note 2: All the photopeak data for Pa-234m and Th-234 gamma rays will be displayed in the following step.

2. Go to the Isotopics Select box and choose Uranium on the right-hand side of the Isotopics page.

Note: Commonly used gamma rays include the following: 63.29, 92.57, 258.18, 742.82, 766.41, and 1001.00 keV.

3. Create the relative efficiency versus energy curve by selecting a minimum of five photopeaks from Pa-234m and Th-234.

Note 1: The isotopic result will be displayed in the following step. Results for U-234 content will be displayed only if the 120.91-keV gamma ray was present in the spectrum.

Note 2: The 120.91-keV gamma is often missing in samples of depleted uranium.

Note 3: If any of the photopeaks used in the calculation have less than 1000 net counts, a warning will come on the screen stating "Poor counting statistics in some peaks may yield inaccurate results." This warning does not mean that the results cannot be calculated; it simply advises that the results may not be as good as desired. Note receipt of this warning in the comments section of the report.

Note 4: If the peaks referred to in the note above are not available or properly identified, an error message will appear on the screen stating "Peak(s) not found to do calculation," and you cannot proceed further with the isotopic calculation.

Note 5: You can save and/or print the report.

4. When the relative efficiency curve has been created to your satisfaction, click the yellow Calculate Isotopics button.

6.7.4 Transmission Corrections Function

When sample matrices are not well known, the ability for SNAP™ to correctly calculate gamma-ray attenuation losses is placed in jeopardy. In such cases, it is advisable to evaluate the attenuating properties of the sample with a multi-gamma transmission source. With the following restrictions, any source can be chosen:

- The source activity and gamma-ray energies must be strong enough to penetrate the entire sample from behind and provide good photopeak statistics in the spectrum.
- The source must have one gamma ray of a lower energy than the sample's assay photo peak and one gamma ray of a higher energy. In general, the two transmission source gamma rays should be reasonably close in energy to the sample gamma ray in order to produce a good estimate (±50 keV).

Analyst:

1. Measure the transmission source alone to establish the unattenuated count rates in the photopeaks of interest.
2. Take a second count with the sample of interest placed between the transmission source and the detector.

Note 1: Both spectra must have the transmission source photopeaks present and identified consistently.

Note 2: The correct identification of matrix materials is unnecessary because the actual transmission data will be used to evaluate attenuation losses. However, the primary wall thickness and material must be entered correctly.

3. When the *.RPu files have been created, then go to the Modeling Data screen and enter the appropriate physical parameters of the measurement.
4. Proceed to the Assay Calculations screen and click the blue Transmission Corrections button.

Note: The *.RPu file will be displayed in the upper window, and the sample file will be displayed in the lower window.

5. Load the *.RPu file from the first measurement of the unattenuated transmission source only (no sample was present).
6. Highlight the lower-energy transmission source photopeak in the upper window, and click the blue Choose Peak 1 button.
7. Highlight the higher-energy transmission source photopeak, and click the blue Choose Peak 2 button.
8. Enter the count time from the transmission source count (which is often shorter in duration than the sample count).
9. Highlight the assay photopeak to be used to generate the nuclide activity in the sample *.RPu file, and click the blue Choose Peak 3 button.
10. Click the yellow Calculate Activites button, and the transmission-corrected results will display.
11. Go to the Reports page to save/print results.

6.7.5 Creating a New Library

This subsection is optional and is performed as needed.

Analyst:

1. Click the gray Edit Libraries button on the Identify Nuclides screen.
2. Type the name of the new library in New Library Name box.
3. Click on the gray New Library button in the Libraries box.
4. Click on the new library to highlight the new library in the Libraries box.

Note: It is possible to choose multiple nuclides by holding down the Shift key while clicking.

5. Choose the nuclides to be in the new library from the Nuclide Selection List box.
6. Click on the gray Add Nuclide(s) To Library button, and the peak energies will appear in the Energies In Library box.

Note: It is a good idea to include Pb-K x-ray, Pb-212, Pb-214, annihilation peak (Annih.), Tl-208, Bi-212, Bi-214, Ac-228, and K-40 in most any new library.

7. If specific energies are to be removed from the new library, then highlight the energies to be removed in The Energies In Library box and click on the gray Remove Nuclide Peak Energy(s) in the Nuclide Peak Energy(s) From Library button.
8. If the new library information is to be removed, then click on the brown Return (Ignore Changes) button to exit the dialog making no changes or remove a library by clicking on the gray Remove Selected Library button.
9. Click on the green Return (Save Changes) button.

6.8 REVIEWING, APPROVING, AND DISTRIBUTING GAMMA SPECTROSCOPY RESULTS

Analyst:

1. Provide a copy of the signed report to the reviewer, including a copy of the logbook notes (see Attachment 5 for a sample report).

Reviewer:

2. Evaluate the quality and accuracy of the complete report.
3. If you find errors, incomplete results, or questionable results, then document the problems and forward the report to the analyst for resolution.

Analyst:

4. Correct all errors and incomplete results and resolve any questionable results to the satisfaction of the reviewer.
5. Provide a copy of the signed, corrected report to the reviewer.

Reviewer:

6. Sign and date on the appropriate lines of the report.

7.0 RECORDS PROCESSING

Analyst or Designee:

1. Forward a copy of the approved gamma spectroscopy report to the waste generator or waste management coordinator.

Note: Under circumstances of extreme urgency, unreviewed results from gamma spectroscopy measurements may be provided to the waste generator or waste management coordinator after verbal or written approval is given by the supervisor. Note that the unreviewed results must clearly be marked as “Draft” or “Preliminary” before distribution.

2. Place an electronic copy of the logbook page, the final report, the spectra used to develop the report, and any interim files in the appropriate network folder Gamma on the WIN domain.

3. Disposition records in accordance with the following:

Record Identification	Record Type Determination	Protection/Storage Method	Processing Instructions
Gamma Spectroscopy Report	QA Record	Supervisor shall implement a reasonable level of protection to prevent loss and degradation.	Records generated by this procedure will be submitted to the Operations Integration Office (OIO-DO) Document Control/Records Management Office and managed in accordance with ADESH-AP-006, *Records Management Plan*.
Gamma Spectroscopy Report copy	Non-record		Destroy when no longer required.

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Tsoulfanidis, N., *Measurement and Detection of Radiation*, McGraw-Hill, Inc., New York (1983). (This reference discusses all types of radiation detectors and associated electronics; includes excellent discussion on solid-angle determination.)

Turner, J.E., *Atoms, Radiation, and Radiation Protection,* Second Edition, John Wiley and Sons, Inc. (1995)

U.S. Department of Health, Education, and Welfare. *Radiological Health Handbook*, Public Health Service, Rockville, MD (1970). (This is a basic reference for personnel in the field of radiation protection.)

Software:

- Genie-2000, Canberra Industries, Inc.
- Maestro®, ORTEC®
- MicroShield®, Grove Engineering
- Nuclide Navigator™, Battelle Memorial Institute

- PeakDoctor, Los Alamos National Laboratory/Pajarito Scientific Corporation
- PHOTCOEF, Applied Inventions Corporation
- RadDecay®, Grove Engineering
- SNAP™, Eberline Services/Pajarito Scientific Corporation

Technical Documents:

- CAL WDP-LLWD WIPP-WAC Equivalence Support Measurements – Sludge, Los Alamos National Laboratory Technical Document EP-TD-2206 (Effective Date: March 21, 2011)
- Error Estimation for Field Gamma Spectroscopy Measurements, Los Alamos National Laboratory Technical Document SWO-TD-0301 (Effective Date: August 24, 2005)
- Matrix Uncertainty Testing for the SNAP Gamma Spectroscopy Modeling Routine, Los Alamos National Laboratory REPORT-SWO-031 (Effective Date: January 14, 2004)
- Pu-238 Activity Concentration Determination for LANL Sludge Drums, Los Alamos National Laboratory Technical Document EP-TD-2202 (Effective Date: April 16, 2009)
- Using Spectral Summing to Determine Radionuclide Activity of LANL Waste Containers, Los Alamos National Laboratory Technical Document EP-TD-2211 (Effective Date: February 6, 2012)
- Validation of Peak Doctor, Robwin, and Maestro Gamma Ray Spectrum Fitting Routines, Los Alamos National Laboratory REPORT-SWO-034 (Effective Date: February 17, 2004)
- WDP-LLWD WIPP-WAC Equivalence Support Measurements, Los Alamos National Laboratory Technical Document EP-TD-2203 (Effective Date: February 26, 2010)

9.0 ATTACHMENTS

Attachment 1: *Definitions and Acronyms*
Attachment 2: *Common Background Peaks and Yields*
Attachment 3: *Common Sample Peaks and Gamma Yields*
Attachment 4: *Logbook*
Attachment 5: *Sample Gamma Spectroscopy Report Format*

ATTACHMENT 1 – DEFINITIONS AND ACRONYMS

Definitions

Background Count: A spectrum collected while all samples or items of interest are absent from the detector's field of view. During background counts, the radiation detector responds to radiation from sources other than the samples or items to be measured. The energies and intensities of background radiation in a background count are assumed to be present during subsequent measurements of samples, items, or containers.

Full Width at Half-Maximum (FWHM): The width of a peak at half of the maximum peak height with the baseline removed.

Quality Control (QC) Count: An energy spectrum collected to quantitatively assess the response of a spectroscopy system to known radiation emitted from a radiation check source.

Sample Count: An energy spectrum collected with the sample, item, or container of interest placed in the detector's field of view.

Spectral Summing: Adding two or more spectra together to provide better counting statistics.

Acronyms

BDR	batch data report
BSE	backscatter energy
CEP	Compton edge peak
EDMS	Electronic Data Management System
FM	FileMaker (database)
FWHM	full width at half-maximum
HPGe	high-purity germanium
keV	kilo-electron volts
LANL	Los Alamos National Laboratory
MDA	minimum detectable activity
MKL	manual knot location
MT	material type
N/A	not applicable
NDA	non-destructive assay
OIO-DO	Operations Integration Office
OJT	on-the-job training

ATTACHMENT 1 – DEFINITIONS AND ACRONYMS CONT.

QA	quality assurance
QC	quality control
RDS	radioassay data sheet
ROI	region of interest
SNAP™	Spectral Nondestructive Assay Platform
SP	step peak
SPF	spectrum parameter file
WF	weighting factor
WM-SVS	Waste Management – Waste Generator Services

ATTACHMENT 2 – COMMON BACKGROUND PEAKS AND YIELDS

Radionuclide	Energy (KeV)	Yield (Fraction)
Pb x-ray	72.81	N/A
Pb x-ray	74.97	N/A
Pb x-ray	84.75[a]	N/A
Pb x-ray	87.30[a]	N/A
Th-234	63.29	0.0484
Th-234[b]	92.57	0.0558
Ra-226	186.11	0.0359
Pb-212	238.58	0.436
Ra-224	240.76	0.039
Pb-214[c]	295.09	0.192
Ac-228	338.42	0.124
Pb-214[c]	351.87	0.371
Tl-208[c]	510.84	0.0776
Annihilation Peak	511	variable
Tl-208[c]	583.02	0.310
Bi-214	609.31	0.461
Cs-137[d]	661.66	0.852
Bi-212	727.25	0.0665
Tl-208[c]	860.30	0.0432
Ac-228	911.21	0.290
Ac-228	968.97	0.174
Bi-214	1120.27	0.150
Bi-214	1238.11	0.0592
K-40	1460.83	0.107
Ac-228	1588.23	0.0360
Bi-212	1620.66	0.0151
Bi-214	1764.49	0.159

[a] Energies are approximate. More than one discrete x-ray energy is actually present.

[b] More than one discrete gamma ray is actually present.

[c] Yield corrected for branching of decay chain.

[d] Gamma rays are actually emitted by Ba-137m (for example, daughter product assumed to be in secular equilibrium with Cs-137).

ATTACHMENT 3 – COMMON SAMPLE PEAKS AND GAMMA YIELDS

Use to Analyze Gamma Spectra from LANL Waste Streams

Radionuclide	Peak Energy (keV)	Yield (Fraction)
Am-241	59.54	0.359
Th-234*	63.29	0.0484
	92.57	0.0558
Np-239	228.19	0.107
	277.60	0.142
Pu-241	148.57	1.89E-6
Pu-239	129.30	6.29E-5
	375.05	1.55E-5
	413.71	1.47E-5
Pu-238	99.86	7.35E-5
	152.68	9.37E-6
U-235	185.74	0.572
U-237	208.00	0.217
Pu-240	160.28	4.09E-6
Pa-233	311.90	0.386
Pa-234m	766.41	0.00294
	1001.00	0.00837
Cs-137	661.66	0.852
Co-60	1173.20	0.999
	1332.50	1.00
Na-22	1274.50	0.999

* More than one discrete gamma ray is actually present.

ATTACHMENT 4 – LOGBOOK

A detailed logbook is maintained for each detector system and/or long-term special project. The logbook is used to track system use and provide a record of acquired data.

Gamma Spectroscopy Measurements

1. Record an entry for each measurement made with the detector.
2. Entries should include relevant information about the measurement.
3. Relevant information for a typical gamma spectroscopy measurement includes, but is not limited to, the following:
   - Detector name
   - Location and date of measurement
   - Filename
   - Customer name
   - An identifier understood by the customer, such as a barcode or other established item number
   - Item description, including physical dimensions and a diagram, as necessary
   - Detector-to-item geometry
   - Gross weight of item and tare weight of container if known
   - Attenuating matrix if known
   - Container wall materials, and wall thickness if a non-standard container
   - Associated QC and background spectra
   - Any points or areas of significantly elevated gamma-ray dose rates, if known.
4. Make entries as specific and descriptive as possible.
5. Make estimates for unknown quantities (e.g., weights of large items that cannot be weighed directly). Clearly label such values as “estimated.”
6. In addition to entries for each acquired spectrum, it may be beneficial for analysis purposes to record general information about the location and any factors that may affect the assay results, for example
   - known sources of background radiation in the area, or possibly in adjacent areas
   - any other information deemed relevant by the operator.
7. Record names of personnel attending the pre-job briefing.
8. Record identifier and calibration due date of certified scale if known.
9. Draw a line across the bottom of the page at the end of the job and initial on the line.

ATTACHMENT 4 – LOGBOOK

Other Detector Activity

Note: A detailed record of these data is critical in tracking down problems that may occur with the detector and providing information that increases accuracy of analysis results.

Other events in the detector's history may require logbook entries, such as

- a newly calibrated detector
- QC check failure
- suspected malfunction
- repair details if done at LANL (repair details done by the manufacturer are located in the detector file on the gamma server).

ATTACHMENT 5 – SAMPLE GAMMA SPECTROSCOPY REPORT FORMAT

WM-SVS
SUMMARY REPORT

Spectroscopy Date: **February 2nd, 2016**

Location: **TA-54 West**

Customer: **Robyn Petersen**

Description: **Assay of one roll-off bin (W821353) – Homer**

Notes:

The purpose of these measurements is to identify and quantify the gamma-emitting radionuclides present in the waste containers.

All relevant technical information and assumptions used to perform these analyses are provided in the following sections of this report.

Estimated errors on the radioassay data sheet are at one standard deviation.

Analyst: Randy Lucero Date: 03/17/16

Reviewer: [signature] Date: 3/21/16

ATTACHMENT 5 – SAMPLE GAMMA SPECTROSCOPY REPORT FORMAT

WM-SVS SUMMARY OF GAMMA SPECTROSCOPY DATA ANALYSIS

Gamma Spectroscopy System: Homer
QC Count Filename(s): 020216hmq1.chn, 020316hmq1.chn
Background Filename(s): 020216hmb1.chn

QUALIFIED SPECTROSCOPISTS COMMONLY UTILIZE THE FOLLOWING TECHNIQUES IN THE PROCESS OF ANALYZING MEASUREMENT DATA. THE USE OF SOME TECHNIQUES IS BASED ON THE PROFESSIONAL JUDGMENT OF THE ANALYST.

Background Stripping: Subtraction of the background spectrum from the item spectrum.

Geometry/Attenuation Corrections: Correction for source-to-detector geometry, and the attenuation of gamma-rays through the waste matrix and container walls.

Multiple Peak Averaging: Averaging of activities over multiple gamma emission peaks from the same radionuclide or radionuclides which are expected to be in equilibrium with one another.

Multiple Geometries: Characterization of the distribution of contamination in a waste item by measuring from multiple sides or positions (this frequently includes rotation of the waste item during the count). This allows the spectroscopist to weight the contamination model accordingly and reduce the overall uncertainty in the assay result.

Automated Reports: Programmed batch routines perform peak searches and calculate net area counts for each spectrum analyzed.

Active Spectrum Review: All spectra are visually reviewed and the final radionuclide peak identifications are performed using the *Table of Radioactive Isotopes* by Browne and Firestone, or an equivalent reference. Energy lines reported in peak summary tables are not necessarily considered valid by the reviewing analyst. Peaks determined as invalid often include naturally occurring radionuclides which were not identified in the background spectrum, or statistically insignificant peaks caused by slight fluctuations in the Compton continuum. Statistically insignificant peaks are identified as "SF", or statistical fluctuations. In addition, valid peaks are occasionally missed by the automated peak search routine. Valid peaks not identified by the automated search routine are manually evaluated by the analyst.

Relative Efficiency: There are some cases where the activity for a nuclide may be calculated using relative efficiency methods. These cases will be denoted with an asterisk (*) in Table 1.

Assumptions/Deviations:

ATTACHMENT 5 – SAMPLE GAMMA SPECTROSCOPY REPORT FORMAT

Page 3 of 9

Radioassay Data Sheet

Assay Conclusion: LLW

MDAs Set with MT and Ref Isotope: PU52 (Pu239), U(NAT) (None)

Container ID:	W821353		*Site ID:*	LANL	
Location:	TA-54 West Bld. 1001		*Procedure:*	EP-DOP-2203, EP-AP-2203	
File Name:	020216hm01.htm		*Software:*	SnapTM v1 13, PeakDoctor v1 1	
Detector:	Homer		*FileID:*	020216hm01.htm	
Assay Date and Time:	2/2/16 12:00 PM		*Assay Method:*	Gamma	
Description:	Roll-off bin		*No. Isotopes:*	10	
Batch Data Report:	LALLW2602		*Item Name:*	htm file	
Fill Height (%):			*Density (kg/L):*		
Net Weight (kg):	1827.3				
Pu Mass (g):	<LLD	±	0.00E+00		
Total Activity (Ci):	<LLD	±	0.00E+00		
TRU Alpha Activity (Ci):	<LLD	±	0.00E+00		
TRU Conc (nCi/g):	<LLD	±	0.00E+00		
LLW Conc (nCi/g):	5.65E+00	±	0.00E+00		
Pu239 Equivalent Activity (Ci):	<LLD	±	0.00E+00		
Pu239 FGE (g):	<LLD	±	0.00E+00		
Decay Heat (W):	<LLD	±	0.00E+00		

Nuclide	Mass (g)	Activity (Ci)	Activity Uncertainty (Ci)	MDA (Ci)
Am241	<LLD	<LLD	0.00E+00	8.80E-04
Cs137	<LLD	<LLD	0.00E+00	5.58E-07
Pu238	<LLD	<LLD	0.00E+00	2.19E-04
Pu239	<LLD	<LLD	0.00E+00	7.48E-03
Pu240	<LLD	<LLD	0.00E+00	1.75E-03
Pu241	<LLD	<LLD	0.00E+00	2.64E-02
Pu242	<LLD	<LLD	0.00E+00	1.01E-07
Sr90	<LLD	<LLD	0.00E+00	5.58E-07
U234	<LLD	<LLD	0.00E+00	1.60E-08
U235	<LLD	<LLD	0.00E+00	2.78E-10

N/S = None Specified

Analyst: [signature] Date: 03/17/16

Reviewer: [signature] Date: 3/21/16

(All Uncertainties are 1 Standard Deviation)

1 of 2

ATTACHMENT 5 – SAMPLE GAMMA SPECTROSCOPY REPORT FORMAT

Page 4 of 9

Radioassay Data Sheet

Assay Conclusion: LLW

MDAs Set with MT and Ref Isotope: PU52 (Pu239), U(NAT) (None)

Container ID:	W821353	*Site ID:*	LANL
Location:	TA-54 West Bld. 1001	*Procedure:*	EP-DOP-2203, EP-AP-2203
File Name:	020216hm01.htm	*Software:*	SnapTM v1.13, PeakDoctor v1.1
Detector:	Homer	*FileID:*	020216hm01.htm
Assay Date and Time:	2/2/16 12:00 PM	*Assay Method:*	Gamma
Description:	Roll-off bin	*No. Isotopes:*	10
Batch Data Report:	LALLW2602	*Item Name:*	htm file
Fill Height (%):		*Density (kg/L):*	

Comments

Unlocked cells depicted by green color coding

Evaluation Data for Analyst and Reviewer

Limit Criteria				
TRU/LLW		100 nCi/g		
PECi		80 Ci		
FGE		200 g		
Correlations				
Suppress All	TRUE			
Suppress U	TRUE			
MDA w/Pu >LLD	TRUE			
Assay Evaluation		Values		
WIPP nCi/g	LLW	<LLD	±	0.00
LLW nCi/g	LLW		5.65 ±	0.00
PECI	<LLD	<LLD	±	0.00
FGE + 2 Sigma	<LLD	<LLD		

ATTACHMENT 5 – SAMPLE GAMMA SPECTROSCOPY REPORT FORMAT

Item: Roll-off bin# W821353
File ID: 020216hm01.RPu

Model
Type: Box
Height (in): 60.00
Width (in): 192.00
Depth (in): 96.00
Volume (ft^3): 640.00

Detector Location
Distance (in): 96.00
Height (in): 30.00
Left of Center (in): 0.00

Detector: Homer
Collimator: Homer: ScooBy @356

Waste Matrix: Cellulose 2004 (100.00%)
Waste Matrix Density (g/cm3): 9.000E-1
Secondary Matrix: N/A
Package Weight (lbs): 4020.00
Packing Efficency: 0.112
Waste Matrix Eff. Density: 1.006E-1
Item Weight: N/A

Wall Material
Primary: Iron 2004
Secondary: None
Tertiary: None

Wall Thickness (in)
Primary: 0.125000
Secondary: 0.000000
Tertiary: 0.000000

Wall Material Density (g/cm3)
Primary: 7.875E+0
Secondary: 0.000E+0
Tertiary: 0.000E+0

Count Time (sec): 7200
Altitude (ft): 7000.00
Rate Loss Correction Factor: 1.000
Lump Correction: None
Thickness (microns): 0

Analyst: Randy Lucero
Notes: BKG subtracted. Net counts displayed are equivalent to the detection limit.

Item: Roll-off bin# W821353
File ID: 020216hm01.RPu

Summary:

Nuclide	Uniform Activity (Ci)	Uniform Conc (nCi/g)	Uniform SNM mass (g)	+2s Error (%)
Pu239	< 7.48E-3	< 4.10E+0	< 1.21E-1	255.09
U235	< 5.53E-7	< 3.03E-4	< 2.56E-1	201.47

Detail.

Nuclide	Energy (keV)	Yield (gps/dps)	Net Counts (counts)	Bkg Counts (counts)	Intrinsic Efficiency (cps/gps)	Uniform Activity (Ci)	Uniform MDA (Ci)	Uniform Conc (nCi/g)	Uniform MDA Conc (nCi/g)	Uniform SNM mass (g)	+2s Error (%)
Pu239	129.29	6.29E-5	297.129	4001	7.632E-1	< 7.48E-3	7.48E-3	< 4.10E+0	4.10E+0	< 1.21E-1	255.09
U235	185.74	5.72E-1	252.935	2889	6.642E-1	< 5.53E-7	5.53E-7	< 3.03E-4	3.03E-4	< 2.56E-1	201.47

ATTACHMENT 5 – SAMPLE GAMMA SPECTROSCOPY REPORT FORMAT

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16hm01.RPu 3/17/2016 2:30:07 PM Page 1

ysis Report for Peak Doctor Version Version 1.1.0.0
of analysis: Feb 04, 2016
in has to be here as a token string for SNAP.
ctor Calibration: Homer
trum ID: 020216hm01
ysis Energy Range: 40.166keV to 1999.9keV

Egy(keV)	FWHM	Area	+/-Area	Background
74.93	0.84	753	110	2811
77.29	0.84	1150	111	2790
185.95	0.88	274	72	1222
238.63	1.11	1341	75	1087
241.97	0.97	494	65	924
295.21	1.15	1260	67	805
338.34	1.06	289	52	604
351.89	1.18	2377	70	640
462.84	1.07	139	42	415
510.79	2.50	3319	83	879
583.11	1.40	1055	52	414
609.26	1.39	3601	72	398
727.25	1.49	336	42	351
768.38	1.48	399	41	322
794.80	1.33	103	35	275
860.79	1.49	181	36	285
911.13	1.71	1092	48	309
934.16	1.78	309	39	310
964.74	1.70	220	37	289
968.96	1.71	710	43	288
1120.32	1.95	1531	51	269
1155.06	2.10	131	37	308
1238.14	1.97	608	42	285
1280.86	2.52	152	35	273
1377.53	1.91	338	30	139
1385.47	1.69	90	24	121
1401.58	2.78	159	31	201
1408.04	2.17	242	29	156
1460.84	2.20	10759	106	143
1509.31	2.27	202	25	107
1582.45	2.48	118	22	93
1588.09	2.49	179	23	91
1592.81	2.49	107	22	91
1621.36	2.08	64	19	72
1630.50	1.79	68	18	60
1661.18	2.53	103	20	79
1729.68	2.07	288	23	58
1764.49	2.45	1613	43	64
1837.69	2.95	61	18	67
1847.35	2.29	193	20	53

ATTACHMENT 5 – SAMPLE GAMMA SPECTROSCOPY REPORT FORMAT

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****

* Peak Analysis *

****

Peak No.	Name	Energy	Branch Ratio	Peak Area	Cont. Counts	Corr. Energy
1	Pb-Kx	74.97	4.62E-01	73	5622	74.970
2	Bi-Ka1	77.11	4.62E-01	200	5580	77.330
3	U235	185.74	5.72E-01	-10	2444	185.986
4	Pb212	238.58	4.36E-01	-363	2174	238.664
5	Pb214	241.92	7.46E-02	-82	1848	242.004
6	Pb214	295.09	1.92E-01	217	1610	295.242
7	Ac228	338.42	1.24E-01	-78	1208	338.371
8	Pb214	351.87	3.71E-01	639	1280	351.920
9	Ac228	463.10	4.60E-02	-4	830	462.866
10	Annih.	511.00	1.00E+00	77	1758	510.814
11	Tl208	583.02	3.10E-01	-88	828	583.132
12	Bi214	609.31	4.61E-01	1185	796	609.281
13	Bi212	727.25	6.65E-02	-15	702	727.267
14	Bi214	768.35	4.88E-02	127	644	768.395
15	Ac228	794.79	4.60E-02	-96	550	794.814
16	Tl208	860.30	4.32E-02	-31	570	860.802
17	Ac228	911.21	2.90E-01	-45	618	911.140
18	Bi214	934.04	3.16E-02	84	620	934.169
19	Ac228	964.64	5.80E-02	-20	578	964.748
20	Ac228	968.97	1.74E-01	14	576	968.968
21	Bi214	1120.27	1.50E-01	578	538	1120.322
22	Bi214	1155.18	1.69E-02	34	616	1155.061
23	Bi214	1238.11	5.92E-02	225	570	1238.138
24	Bi214	1280.95	1.47E-02	43	546	1280.857
25	Bi214	1377.66	4.02E-02	29	278	1377.523
26	Bi214	1385.30	7.80E-03	90	242	1385.463
27	Bi214	1401.48	1.39E-02	59	402	1401.572
28	Bi214	1407.97	2.48E-02	89	312	1408.032
29	K40	1460.83	1.07E-01	194	286	1460.830
30	Bi214	1509.22	2.19E-02	50	214	1509.298
31	Bi214	1583.22	7.20E-03	118	186	1582.436
32	Ac228	1588.23	3.60E-02	-44	182	1588.076
33	D.Esc.3	1592.35	1.00E+00	7	182	1592.795
34	Bi212	1620.66	1.51E-02	-20	144	1621.344
35	Ac228	1630.47	1.95E-02	-7	120	1630.484
36	Bi214	1661.26	1.15E-02	56	158	1661.163
37	Bi214	1729.58	3.05E-02	114	116	1729.661
38	Bi214	1764.49	1.59E-01	517	128	1764.469
39	Bi214	1838.40	3.83E-03	61	134	1837.667
40	Bi214	1847.41	2.12E-02	40	106	1847.326

ATTACHMENT 5 – SAMPLE GAMMA SPECTROSCOPY REPORT FORMAT

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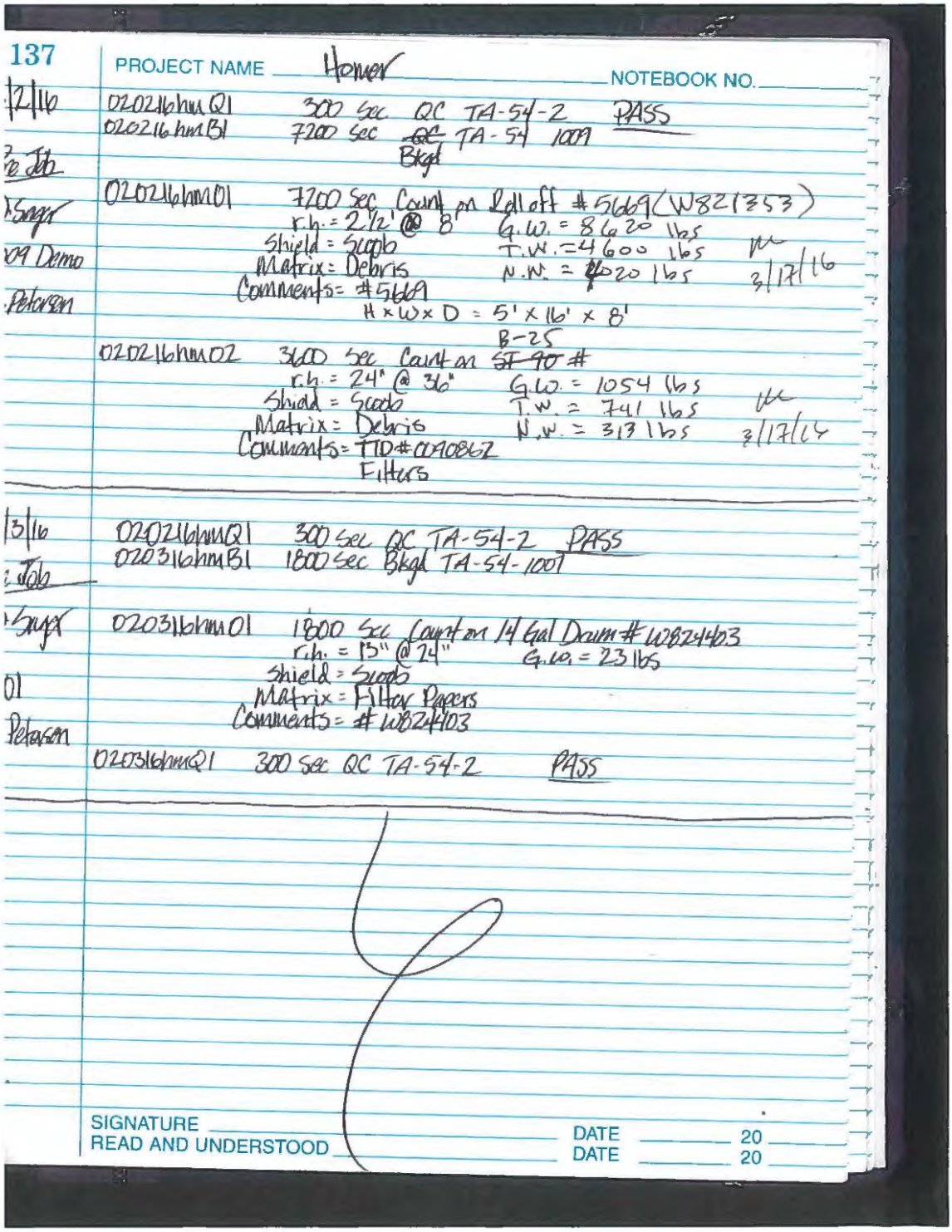

137

PROJECT NAME Hower NOTEBOOK NO.

2/16
Job
Sager
09 Demo
Peterson

020216hmQ1 300 Sec QC TA-54-2 PASS
020216hmB1 7200 Sec ~~QC~~ Bkgd TA-54 1009

020216hm01 7200 Sec Count on Roll off #5669 (W821353)
r.h. = 2½' @ 8' G.W. = 8620 lbs
Shield = Stubb T.W. = 4600 lbs
Matrix = Debris N.W. = 4020 lbs
Comments = #5669 3/17/16
H x W x D = 5' x 16' x 8'
B-25

020216hm02 3600 Sec Count on ~~ST 90~~ #
r.h. = 24" @ 36" G.W. = 1054 lbs
Shield = Stubb T.W. = 741 lbs
Matrix = Debris N.W. = 313 lbs 3/17/16
Comments = TLD# 0010867
Filters

3/16
Job
Sager
01
Peterson

020216hmQ1 300 Sec QC TA-54-2 PASS
020316hmB1 1800 Sec Bkgd TA-54-1001

020316hm01 1800 Sec Count on 14 Gal Drum # W824403
r.h. = 15" @ 24" G.W. = 23 lbs
Shield = Stubb
Matrix = Filter Papers
Comments = # W824403

020316hmQ1 300 Sec QC TA-54-2 PASS

SIGNATURE _____ DATE _____ 20 _____
READ AND UNDERSTOOD _____ DATE _____ 20 _____